

**Figure S5.** Composite of mapped reads across all samples for exon 3b. The depth of mapped reads is indicated by the gray histogram in the upper panel, while *HTR2A* gene structure is depicted in the lower panel (3'-to-5' direction from left-to-right). The histogram depicts exon 3b starting adjacent to the 3' splice acceptor site and continuing approximately 1.2 kb to the poly-A signal cluster, proximal to where read depth noticeably decreases. Canonical and non-canonical poly-A sites are marked in the lower panel as red dots. *Note:* read depth is presented in linear scale.